

Replacement Sheet

(-40)																			
1																			
Met	Gly	Arg	Pro	Leu	His	Leu	Val	Leu	Leu	Ser	Ala	Ser	Leu	Ala	Gly	Leu	Leu	Leu	
ATG	GGG	CGC	CCA	CTG	CAC	CTC	GTC	CTG	CTC	AGT	GCC	TCC	CTG	GCT	GGC	CTC	CTG	CTG	
		9			18			27			36			45			54		
															(-4)				
															(-1)				
Leu	Gly	Glu	Ser	Leu	Phe	Ile	Arg	Arg	Glu	Gln	Ala	Asn	Asn	Ile	Leu	Ala	Arg	Val	Thr
CTC	GGG	GAA	AGT	CTG	TTC	ATC	CGC	AGG	GAG	CAG	GCC	AAC	AAC	ATC	CTG	GCG	AGG	GTC	ACG
		66			75			84			93			102			111		120
(+1)																			
41																			
Ala	Asn	Ser	Phe	Leu	Glu	Glu	Met	Lys	Lys	Gly	His	Leu	Glu	Arg	Glu	Cys	Met	Glu	Glu
GCC	AAT	TCC	TTT	CTT	GAA	GAG	ATG	AAG	AAA	GGA	CAC	CTC	GAA	AGA	GAG	TGC	ATG	GAA	GAG
		129			138			147			156			165			174		183
Cys	Ser	Tyr	Glu	Glu	Ala	Arg	Glu	Val	Phe	Glu	Asp	Ser	Asp	Lys	Thr	Asn	Glu	Phe	Trp
TGC	TCA	TAC	GAA	GAG	GCC	CGC	GAG	GTC	TTT	GAG	GAC	AGC	GAC	AAG	ACG	AAT	GAA	TTC	TGG
		192			201			210			219			228			237		246
Lys	Tyr	Lys	Asp	Gly	Asp	Gln	Cys	Glu	Thr	Ser	Pro	Cys	Gln	Asn	Gln	Gly	Lys	Cys	Lys
AAA	TAC	AAA	GAT	GGC	GAC	CAG	TGT	GAG	ACC	AGT	CCT	TGC	CAG	AAC	CAG	GGC	AAA	TGT	AAA
		255			264			273			282			291			300		309
Gly	Leu	Gly	Glu	Tyr	Thr	Cys	Thr	Cys	Leu	Glu	Gly	Phe	Glu	Gly	Lys	Asn	Cys	Glu	Leu
GGC	CTC	GGG	GAA	TAC	ACC	TGC	ACC	TGT	TTA	GAA	GGA	TTC	GAA	GGC	AAA	AAC	TGT	GAA	TTA
		318			327			336			345			354			363		372
Thr	Arg	Lys	Leu	Cys	Ser	Leu	Asp	Asn	Gly	Asp	Cys	Asp	Gln	Phe	Cys	His	Glu	Glu	Gln
ACA	CGG	AAG	CTC	TGC	AGC	CTG	GAC	AAC	GGG	GAC	TGT	GAC	CAG	TTC	TGC	CAC	GAG	GAA	CAG
		381			390			399			408			417			426		435
Ser	Val	Val	Cys	Ser	Cys	Ala	Arg	Gly	Tyr	Thr	Leu	Ala	Asp	Asn	Gly	Lys	Ala	Cys	Ile
TCT	GTG	GTG	TGC	TCC	TGC	GCC	CGC	GGG	TAC	ACC	CTG	GCT	GAC	AAC	GGC	AAG	GCC	TGC	ATT
		444			453			462			471			480			489		498
Thr	Gly	Pro	Tyr	Pro	Cys	Gly	Lys	Gln	Thr	Leu	Glu	Arg	Arg	Lys	Arg	Ser	Val	Ala	Gln
ACA	GGG	CCC	TAC	CCC	TGT	GGG	AAA	CAG	ACC	CTG	GAA	CGC	AGG	AAG	AGG	TCA	GTG	GCC	CAG
		507			516			525			534			543			552		561
Thr	Ser	Ser	Ser	Gly	Glu	Ala	Pro	Asp	Ser	Ile	Thr	Trp	Lys	Pro	Tyr	Asp	Ala	Ala	Asp
ACC	AGC	AGC	AGC	GGG	GAG	GCC	CCT	GAC	AGC	ATC	ACA	TGG	AAG	CCA	TAT	GAT	GCA	GCC	GAC
		570			579			588			597			606			615		624
															R6				
															229				
Asp	Pro	Thr	Glu	Asn	Pro	Phe	Asp	Leu	Leu	Asp	Phe	Asn	Gln	Thr	Gln	Pro	Glu	Arg	Gly
GAC	CCC	ACC	GAG	AAC	CCC	TTC	GAC	CTG	CTT	GAC	TTC	AAC	CAG	ACG	CAG	CCT	GAG	AGG	GGC
		633			642			651			660			669			678		687
R5	R4	R3	R2					R1											
															234				
															235				
Asn	Asn	Leu	Thr	Arg	Ile	Val	Gly	Gly	Gln	Glu	Cys	Lys	Asp	Gly	Glu	Cys	Pro	Trp	Gln
AAC	AAC	CTC	ACC	AGG	ATC	GTG	GGA	GGC	CAG	GAA	TGC	AAG	GAC	GGG	GAG	TGT	CCC	TGG	CAG
		696			705			714			723			732			741		750

Fig. 1A

Leu	Leu	Ile	Asn	Glu	Glu	Asn	Glu	Gly	Phe	Cys	Gly	Gly	Thr	Ile	Leu	Ser	Glu	Phe	Tyr	Ile
CTG	CTC	ATC	AAT	GAG	GAA	AAC	GAG	GGT	TTC	TGT	GGT	GGA	ACT	ATT	CTG	AGC	GAG	TTC	TAC	ATC
		759			768			777			786			795			804			813
Leu	Thr	Ala	Ala	His	Cys	Leu	Tyr	Gln	Ala	Lys	Arg	Phe	Lys	Val	Arg	Val	Gly	Asp	Arg	Asn
CTA	ACG	GCA	GCC	CAC	TGT	CTC	TAC	CAA	GCC	AAG	AGA	TTC	AAG	GTG	AGG	GTA	GGG	GAC	CGG	AAC
		822			831			840			849			858			867			876
Thr	Glu	Gln	Glu	Glu	Gly	Gly	Glu	Ala	Val	His	Glu	Val	Glu	Val	Val	Ile	Lys	His	Asn	Arg
ACG	GAG	CAG	GAG	GAG	GGC	GGT	GAG	GCG	GTG	CAC	GAG	GTG	GAG	GTG	GTC	ATC	AAG	CAC	AAC	CGG
		885			894			903			912			921			930			939
Phe	Thr	Lys	Glu	Thr	Tyr	Asp	Phe	Asp	Ile	Ala	Val	Leu	Arg	Leu	Lys	Thr	Pro	Ile	Thr	Phe
TTC	ACA	AAG	GAG	ACC	TAT	GAC	TTC	GAC	ATC	GCC	GTG	CTC	CGG	CTC	AAG	ACC	CCC	ATC	ACC	TTC
		948			957			966			975			984			993			1002
Arg	Met	Asn	Val	Ala	Pro	Ala	Cys	Leu	Pro	Glu	Arg	Asp	Trp	Ala	Glu	Ser	Thr	Leu	Met	Thr
CGC	ATG	AAC	GTG	GCG	CCT	GCC	TGC	CTC	CCC	GAG	CGT	GAC	TGG	GCC	GAG	TCC	ACG	CTG	ATG	ACG
		1011			1020			1029			1038			1047			1056			1065
Gln	Lys	Thr	Gly	Ile	Val	Ser	Gly	Phe	Gly	Arg	Thr	His	Glu	Lys	Gly	Arg	Gln	Ser	Thr	Arg
CAG	AAG	ACG	GGG	ATT	GTG	AGC	GGC	TTC	GGG	CGC	ACC	CAC	GAG	AAG	GGC	CGG	CAG	TCC	ACC	AGG
		1074			1083			1092			1101			1110			1119			1128
Leu	Lys	Met	Leu	Glu	Val	Pro	Tyr	Val	Asp	Arg	Asn	Ser	Cys	Lys	Leu	Ser	Ser	Ser	Phe	Ile
CTC	AAG	ATG	CTG	GAG	GTG	CCC	TAC	GTG	GAC	CGC	AAC	AGC	TGC	AAG	CTG	TCC	AGC	AGC	TTC	ATC
		1137			1146			1155			1164			1173			1182			1191
Ile	Thr	Gln	Asn	Met	Phe	Cys	Ala	Gly	Tyr	Asp	Thr	Lys	Gln	Glu	Asp	Ala	Cys	Gln	Gly	Asp
ATC	ACC	CAG	AAC	ATG	TTC	TGT	GCC	GGC	TAC	GAC	ACC	AAG	CAG	GAG	GAT	GCC	TGC	CAG	GGG	GAC
		1200			1209			1218			1227			1236			1245			1254
Ser	Gly	Gly	Pro	His	Val	Thr	Arg	Phe	Lys	Asp	Thr	Tyr	Phe	Val	Thr	Gly	Ile	Val	Ser	Trp
AGC	GGG	GGC	CCG	CAC	GTC	ACC	CGC	TTC	AAG	GAC	ACC	TAC	TTC	GTG	ACA	GGC	ATC	GTC	AGC	TGG
		1263			1272			1281			1290			1299			1308			1317
Gly	Glu	Ser	Cys	Ala	Arg	Lys	Gly	Lys	Tyr	Gly	Ile	Tyr	Thr	Lys	Val	Thr	Ala	Phe	Leu	Lys
GGA	GAG	AGC	TGT	GCC	CGT	AAG	GGG	AAG	TAC	GGG	ATC	TAC	ACC	AAG	GTC	ACC	GCC	TTC	CTC	AAG
		1326			1335			1344			1353			1362			1371			1380
Trp	Ile	Asp	Arg	Ser	Met	Lys	Thr	Arg	Gly	Leu	Pro	Lys	Ala	Lys	Ser					

Pre-/Propeptid
'Connecting' Tripeptide
Activation Peptide

Fig. 1B